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First record of the family Ptilocerembiidae (Insecta, Embioptera) from China, with morphological and molecular characterization of a new species

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Abstract

We report the first record of the webspinner family Ptilocerembiidae Miller & Edgerly, 2012, from China, represented by a new species, *Ptilocerembia qiului* **sp. nov.**, discovered in Yunnan Province. Detailed morphological examination, particularly the comparative analysis of male terminalia, clearly distinguishes this species from its congeners. The complete mitochondrial genome of *P. qiului* **sp. nov.** (15,443 bp) was sequenced, exhibiting the canonical insect gene order with strong A+T bias but showing the absence of two tRNAs (trnV and trnS2). Notably, we detected novel tandem repeats between trnI and trnQ, a feature not reported from other sequenced embiopteran mitogenomes. All protein-coding genes evolve under purifying selection, with COX1 showing the highest conservation. DNA barcoding (COX1) and phylogenetic analyses further support species delimitation in *Ptilocerembia*, with interspecific divergences between the new species and other *Ptilocerembia* (12.6–17.6%) far exceeding frequently used intraspecific thresholds (~2%). The discovery extends the known distribution range of Ptilocerembiidae northeastward to southwestern China. Our integrative morphological and molecular framework highlights the previously underestimated species richness in *Ptilocerembia* and provides the first mitogenomic insights into Ptilocerembiidae.

Key Words

mitogenomics, *Ptilocerembia*, species delimitation, taxonomy, webspinners

Introduction

The monogeneric webspinner family Ptilocerembiidae Miller & Edgerly, 2012, was established based on the genus *Ptilocerembia* Friederichs, 1923, originally described from Indonesia (type species: *Ptilocerembia roepkei* Friederichs, 1923) (Miller et al. 2012). Historically, *Ptilocerembia* was placed in Notoligotomidae together with the eastern Australian genus *Notoligotoma* Davis, 1936 (Davis 1936; Ross 1963), but molecular phylogenetic analysis recovered it as a distinct lineage (Miller et al. 2012). Miller et al. (2012) thus erected the family Ptilocerembiidae for *Ptilocerembia*. Subsequently, Poolprasert and Edgerly (2014) provided morphological descriptions and biological and distributional information on four new species of *Ptilocerembia* from Thailand, including *Ptilocerembia catherinae* Poolprasert & Edgerly, 2014; *P. rossi* Poolprasert & Edgerly, 2014; *P. senathami* Poolprasert & Edgerly, 2014; and *P. thaidina* Poolprasert & Edgerly, 2014. The males of Ptilocerembiidae/*Ptilocerembia* are characterized by antennae with long setae and white distal segments, distinct wing venation with the anterior media vein forked, densely setose hind basitarsi with a single papilla, an obliquely cleft tergite X, and elaborated male terminalia (e.g., left tergal process short, medial flap with a hooked prong, and fused left cercomeres) (Miller et al. 2012; Poolprasert and Edgerly 2014). Mitochondrial DNA barcoding (COX1) has also been shown to be effective for distinguishing *Ptilocerembia* species (Poolprasert et al. 2017, 2021).

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To date, all known *Ptilocerembia* species are known from Indonesia, Myanmar, and Thailand (Miller et al. 2012; Poolprasert and Edgerly 2014). In this study, we report the first record of *Ptilocerembia* and the family Ptilocerembiidae from China. We describe *Ptilocerembia qiului* sp. nov. from Yunnan Province, provide detailed morphological characters, and present its complete mitochondrial genome (mitogenome). In addition, we compare the COX1 barcode of the new species with published *Ptilocerembia* sequences to delimit species boundaries. This integrative approach yields novel data on the taxonomy, phylogeny, and biogeography of *Ptilocerembia* and Ptilocerembiidae.

Material and methods

Sample collection and morphological examination

The specimens were manually collected from the road surface in Yingpan, Ailao Mountain, Yunnan Province, China (23.9901°N, 101.5476°E; altitude 2000 m) on 23 May 2018. They were preserved in 75% ethanol. A morphological study was conducted under an SZM45 stereomicroscope. Images of habitus and structures were taken with a Canon EOS 5DSR digital camera and an MP-E 65 mm macro lens and processed with Adobe Photoshop v2025. The distribution map was produced using QGIS v3.40.11. Morphological terminology follows Ross (2007) and Poolprasert and Edgerly (2014). The holotype and paratype are deposited in the Insect Collection of Jiangsu University of Science and Technology (**ICJUST**), Zhenjiang, China.

Mitogenome sequencing and assembly

Genomic DNA was extracted from a single leg of the holotype (genseq-1) using the Wizard SV Genomic DNA Purification System Kit (Promega, USA). A paired-end Illumina library (~400 bp insert) was prepared and sequenced (2×150 bp) on the Illumina HiSeq X platform (Annoroad Gene Technology, China). Raw reads were quality-filtered (removing low-quality and short reads), yielding 1.56 Gb of clean data. The mitogenome was assembled independently using GETORGANELLE v1.7.4 and MITOZ v3.6 pipelines (Meng et al. 2019; Jin et al. 2020). The consistency of the two assemblies was confirmed by manual checking. The complete mitogenome sequence was deposited in GenBank with accession number PX232380.

Mitogenome annotation and analysis

Annotation was performed with MITOS2 (Bernt et al. 2013) and by comparison to published embiopteran mitogenomes. Boundaries of protein-coding genes (PCGs) were confirmed by ORF FINDER (NCBI). The circular mitogenome map was visualized using PROKSEE (Grant et al. 2023). We calculated nucleotide composition, codon usage, and relative synonymous codon usage (RSCU) with MEGA11 (Tamura et al. 2021). Pairwise genetic distances (K2P) for COX1 genes and synonymous (Ks) and nonsynonymous (Ka) substitution rates between genes of sequenced webspinners and the outgroup *Phasmotaenia lanyuhensis* Huang & Brock, 2001 (Huang and Brock 2001; GenBank No. PP536087) were computed using MEGA11 and KAKS_CALCULATOR v3.0 (Zhang 2022), respectively. Tandem repeats in the mitogenome were identified using Tandem Repeats Finder (Benson 1999).

Molecular species delimitation and phylogenetic analysis

The COX1 barcode was extracted from the newly sequenced mitogenome. We downloaded all six available *Ptilocerembia* COX1 sequences from GenBank (Miller et al. 2012; Poolprasert et al. 2017, 2021) and aligned them with the new sequence. *Aposthonia borneensis* (Hagen, 1885) (Oligotomidae) was used as an outgroup. Genetic distances (K2P) and a Neighbor-Joining (NJ) tree were generated in MEGA11 (Tamura et al. 2021) using pairwise deletion (gaps removed) and 1000 bootstrap replicates. Maximum likelihood (ML) and Bayesian inference (BI) phylogenies were estimated based on the COX1 alignment. The best-fit nucleotide substitution model was selected by MODELFINDER (Kalyaanamoorthy et al. 2017). BI analysis was run in MRBAYES v3.2.6 (Ronquist et al. 2012) under the GTR+G+F model (2 parallel runs, 5000000 generations), in which the initial 25% of sampled data were discarded as burn-in. ML analysis was performed in IQ-TREE v2.2.0 (Nguyen et al. 2015) under the TIM2+G4+F model for 1000 ultrafast (Minh et al. 2013) bootstraps, as well as the Shimodaira–Hasegawa–like approximate likelihood-ratio test (Guindon et al. 2010). Trees were visualized in FIGTREE v1.4.3.

Results

***Ptilocerembia qiului* sp. nov.**

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Type locality. China, Yunnan Province: Yuxi City, Ailao Mountain, Yingpan, 23.9901°N, 101.5476°E (Fig. 1), 2000 m, on road surface, 23 May 2018.V.23; L. Qiu leg.

Type specimens. ***Holotype*:** • ♂, in alcohol. Original label: "China, Yunnan, Yuxi, Ailao Mountain, Yingpan, 23.9901°N, 101.5476°E, 2000 m, 23 May 2018.V.23, L Qiu", "HOLOTYPE / *Ptilocerembia qiului* sp. nov. / Det. Chen" (ICJUST). ***Paratype*:** • 1♂, with same collection event label as the holotype and additional la-

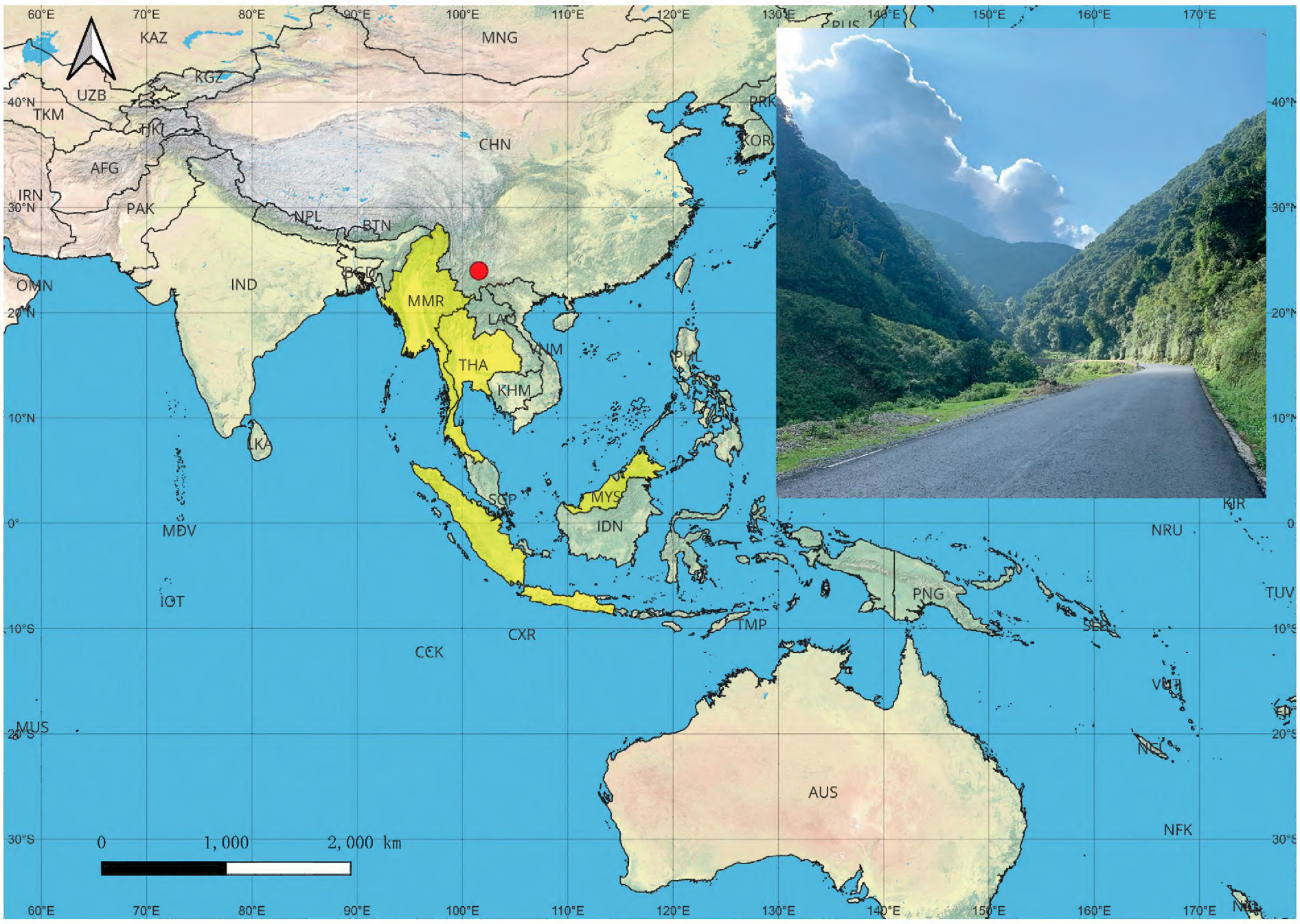

Figure 1. General distribution of *Ptilocerembia* species. Inset: habitat of *Ptilocerembia qiului* sp. nov. in Mt. Ailaoshan, Yunnan Province, China. The type locality of the new species is indicated by a red dot, while the distribution of other species is indicated by yellow.

bel "PARATYPE / *Ptilocerembia qiului* sp. nov. / Det. Chen" (ICJUST).

Diagnosis. *Ptilocerembia qiului* sp. nov. is assigned to the genus *Ptilocerembia* of family Ptilocerembiidae by the antennae with long erect setae and white distal segments, bifurcated MA in all wings, hind basitarsus with dense ventral setae and only one papilla, tergite X obliquely divided into two unequal sclerites with the area between the hemitergites depressed, MF with a hook, elongated HP, and the fused left cercomeres (Miller et al. 2012; Poolprasert and Edgerly 2014). Among the five known species of *Ptilocerembia* (see Suppl. material 1: table S1), *P. qiului* sp. nov. is the most similar to *P. catherinae* based on the 10R with a median convex along left margin, MF with a raised nodule near base of EP, and LC1 with a large echinulate nodule (Poolprasert and Edgerly 2014). However, *P. qiului* sp. nov. can be distinguished from *P. catherinae* by the submentum with anterior margin truncate (concave in *P. catherinae*), MS with broad right half (absent in *P. catherinae* but similar to that of *P. rossi*), 10LP and 10 RP broad (narrow in *P. catherinae* and other species), HP elongated and specialized apically (relatively short and simple in *P. catherinae* and other species) (Friederichs 1923; Poolprasert and Edgerly 2014). The dichotomous key in Poolprasert and Edgerly (2014) could separate *P. catherinae* as well as its similar species, *P. qiului* sp. nov. from other congeners.

Description. Male: Body length (from anterior of maxillary palps to cercal apex) ca. 15 mm; color pale to brown (Fig. 2A, B).

Antennae at least 26-segmented, most segments brown and covered by long erect setae, distal segments pale (Fig. 2C). Head capsule dark brown (Fig. 3A, B), near 1.5 times longer than wide, with reticular pigmentation on posterior 1/3. Eyes small, sides behind eyes rounded, gradually converging posteriorly. Clypeus broad, pale brown; labrum semicircular, dark medially, pale laterally. Maxillary palpi dark brown, five-segmented; labial palpi brown and short, three-segmented. Submentum dark brown, subquadrate, slightly wider than long, anterior margin truncate, posterior margin slightly concave, lateral margins slightly convex.

Prothorax brown (Fig. 3A), subquadrate, slightly wider posteriorly, much shorter and narrower than head, with subequal length and width, surface with deep transverse and longitudinal grooves. Meso- and metathorax generally brown, width subequal to head. Legs brown; hind basitarsus with single ventral papilla (Fig. 3C). Wings pale brown (Fig. 4), with longitudinal pale stripes; MA of all wings forked subbasally.

Abdomen dark brown (Figs 2, 5). Terminalia with tenth abdominal tergite completely cleft, hemitergites separated basally (Fig. 5A–E). MS transverse, sinuate, near fusiform, with a posterior notch on right half. Hemitergite

Figure 2. *Ptilocerembia qiului* sp. nov., male holotype. **A.** Habitus, dorsal view; **B.** Habitus, ventral view; **C.** Distal antennal segments, dorsal view. Scale bars: 1 mm.

10L broad, subtrapezoidal, left margin expanded to ventral side; 10LP constricted basally, right margin rounded, left margin greatly projected leftward medially, apex blunt and curved leftward. 10R broad throughout, inner margin sinuate, with a median convex; MF with a long sickle-shaped hook (EP) and a raised nodule; 10RP broad, subquadrate, apex with left angle pointed and right angle notched. LPPT produced as a subtriangular thin sclerite beneath 10L, sharp LPPT-P pointing backwards. LC1 tubular basally, elongated, inner margin with a large echinulate lobe apically. LC2 shorter than LC1, subconical, basal fusion with LC1 slightly constricted. Right cercus slightly longer than left cercus; RC1 slightly shorter than RC2, both covered with long setae and tapering towards apex. H broad (Fig. 5F, G), rounded, lateral margins obliquely convex; a slender curved sclerite present posterolateral to H. HP near as long as H; right margin mostly straight except expanded basally and convex apically; left margin convex at basal half, forming a denticulate ridge at apical half.

Etymology. The species is named after its collector, Dr. Lu Qiu (Mianyang, Sichuan, China).

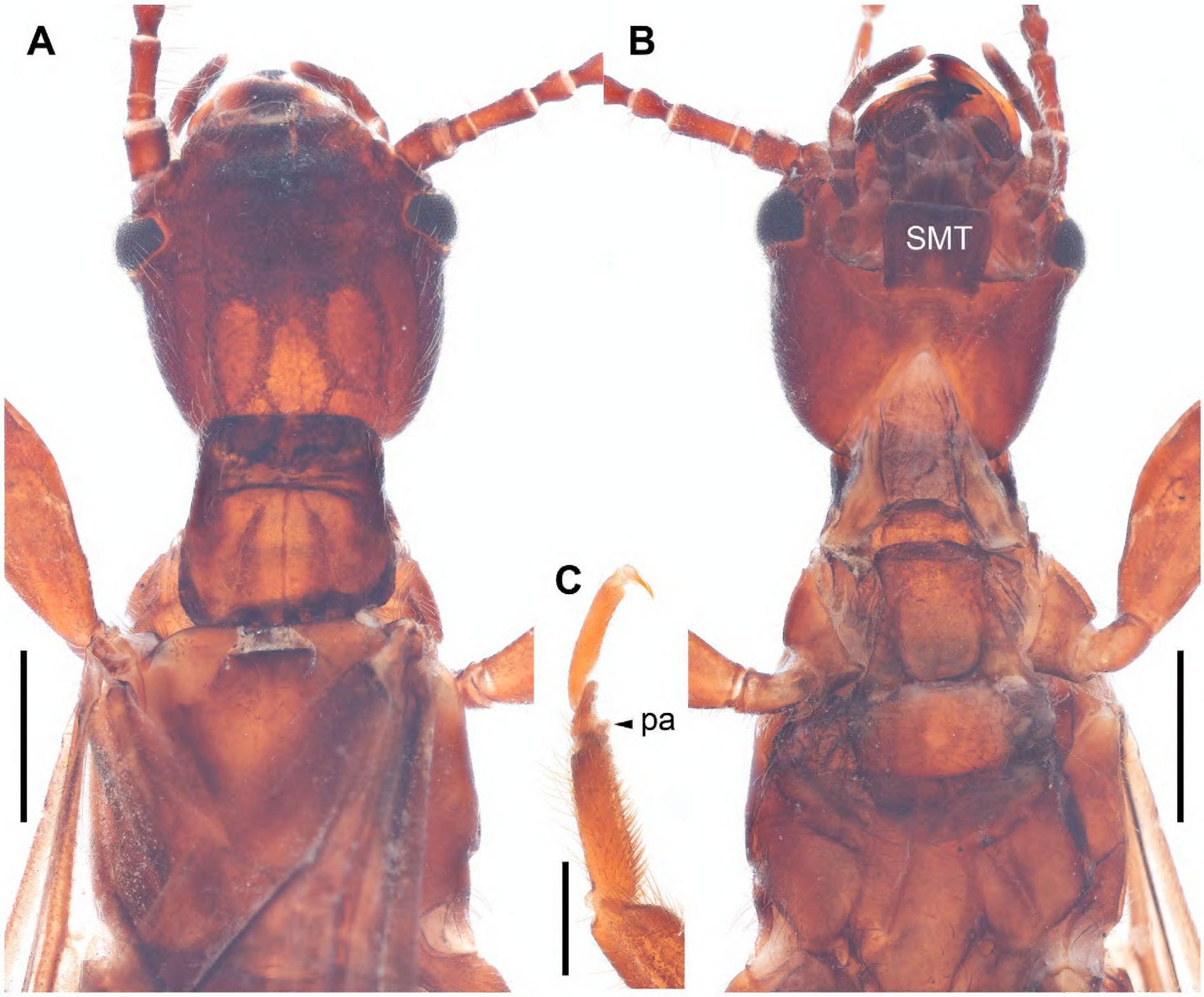

Figure 3. *Ptilocerembia qiului* sp. nov., male holotype. **A.** Head and thorax, dorsal view; **B.** Head and thorax, ventral view; **C.** Right hind tarsus, dorsal view. Abbreviations: pa – papilla; SMT – submentum. Scale bars: 1 mm (**A** and **B**); 0.5 mm (**C**).

Distribution. China: Yunnan Province.

Biology. The specimens were collected at a high-elevation site in the Ailao Mountain region, situated at the transitional boundary between the Yungui Plateau and the Hengduan Mountains. This area serves as a climatic divide between the Pacific Southeast Monsoon and the Indian Ocean Southwest Monsoon systems. The region experiences a subtropical montane climate characterized by cool annual temperatures, with mild summer conditions and cold winters. Precipitation is abundant and seasonally concentrated, with most rainfall occurring during an extended rainy season, while humidity remains consistently high throughout much of the year. The vegetation surrounding the habitat is dominated by extensive mid-elevation moist evergreen broad-leaved forests, recognized as one of China's most significant subtropical montane wet evergreen broad-leaved forest ecosystems. These forests are primarily composed of species from the Fagaceae, Theaceae, Lauraceae, and Magnoliaceae and feature a rich diversity of epiphytes (including mosses and ferns) and lianas. This structurally complex, humid evergreen forest, combined with persistent mist and steep elevational variation, creates stable micro-habitats such as bark crevices, leaf-litter zones, and humid canopy niches that are favorable for webspinners. Given the pronounced vertical climate stratification of the region, the new species may occupy a narrow elevational range with specific humidity, canopy cover, and litter-substrate conditions. Future field studies targeting mid-montane evergreen forest corridors in the Indochina–Yunnan region may reveal a broader distribution of the genus across similar habitats.

Mitogenome characters

The complete mitogenome of *P. qiului* sp. nov. is 15,443 bp in length (GenBank accession No. PX232380), which is slightly smaller than other reported webspinner mitogenomes (typically ~15.7–17.3 kb). It is a circular molecule comprising 13 protein-coding genes (PCGs), 20 tRNA genes, and 2 rRNA genes, plus the A+T-rich

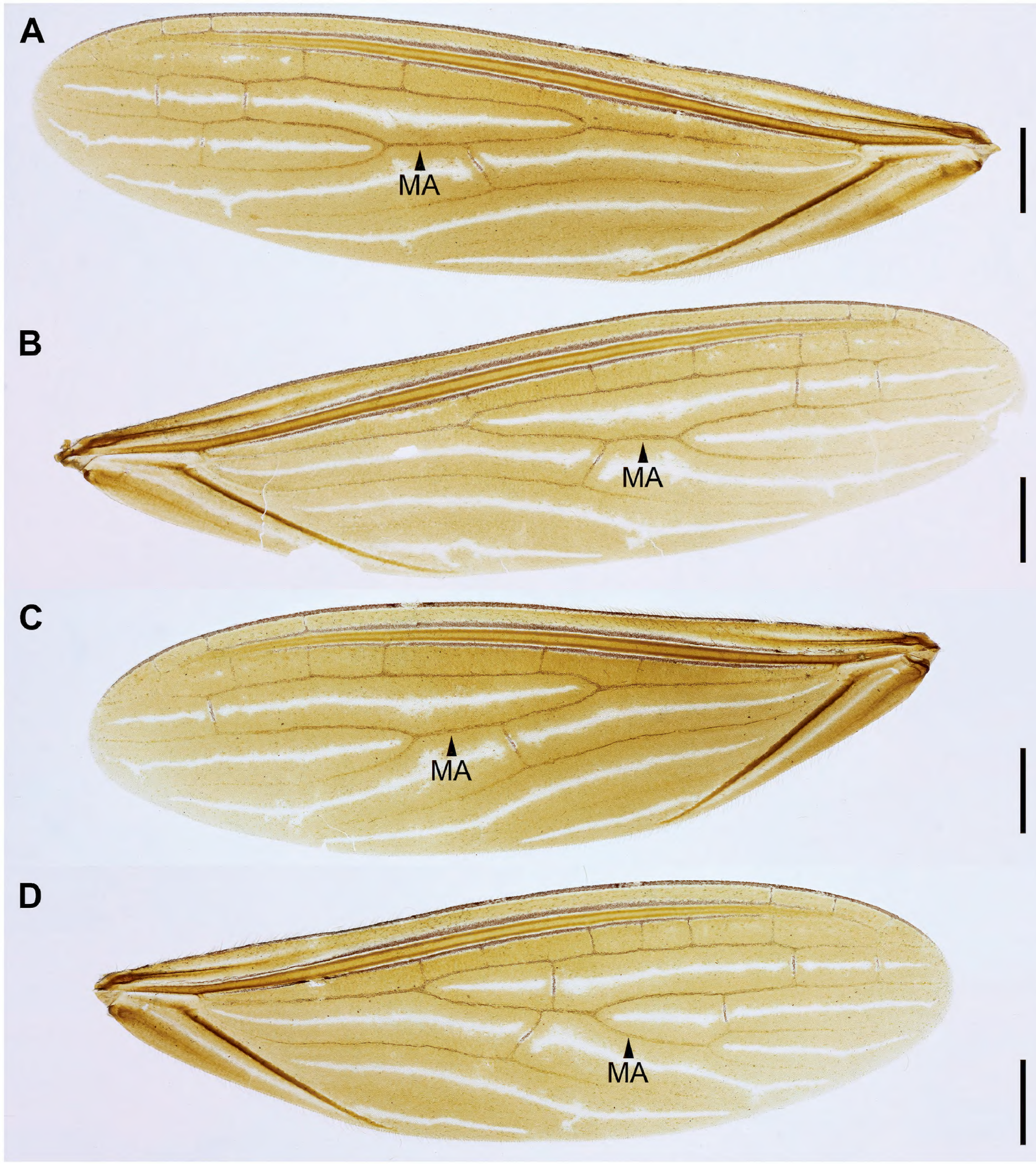

Figure 4. *Ptilocerembia qiului* sp. nov., male holotype. **A.** Left forewing, dorsal view; **B.** Right forewing, dorsal view; **C.** Left hind wing, dorsal view; **D.** Right hind wing, dorsal view. Abbreviation: MA – anterior media. Scale bars: 1 mm.

control region (Fig. 6). Two tRNAs, tRNA-Val (trnV) and tRNA-Ser(UGA) (trnS2), are missing (a feature not seen in other embiopteran mitogenomes). The gene order is the canonical insect arrangement as in *Drosophila yakuba* Burla (1954) (Clary and Wolstenholme 1985), with no rearrangements compared to the ancestral pattern (see Suppl. material 1: table S2). Base composition is strongly A+T-biased (A 39.2%, T 25.1%, G 7.8%, C 27.9%).

A notable feature is the presence of ~5.4 tandem repeat units in the intergenic region between tRNA-Ile and tRNA-Gln. Such repeated sequences have not been reported in other sequenced embiopteran mitogenomes. Tandem Repeats Finder analysis confirmed these repeats (Benson 1999), whereas the control region itself contains no repeated sequences.

Most PCGs use standard invertebrate start codons (ATA, ATG, ATT) and terminate with TAA; six genes (COX1, COX2, COX3, ND1, ND4, ND5) end with an incomplete stop codon (single T), which is presumed to be completed by post-transcriptional polyadenylation. Relative synonymous codon usage (RSCU) analysis shows a

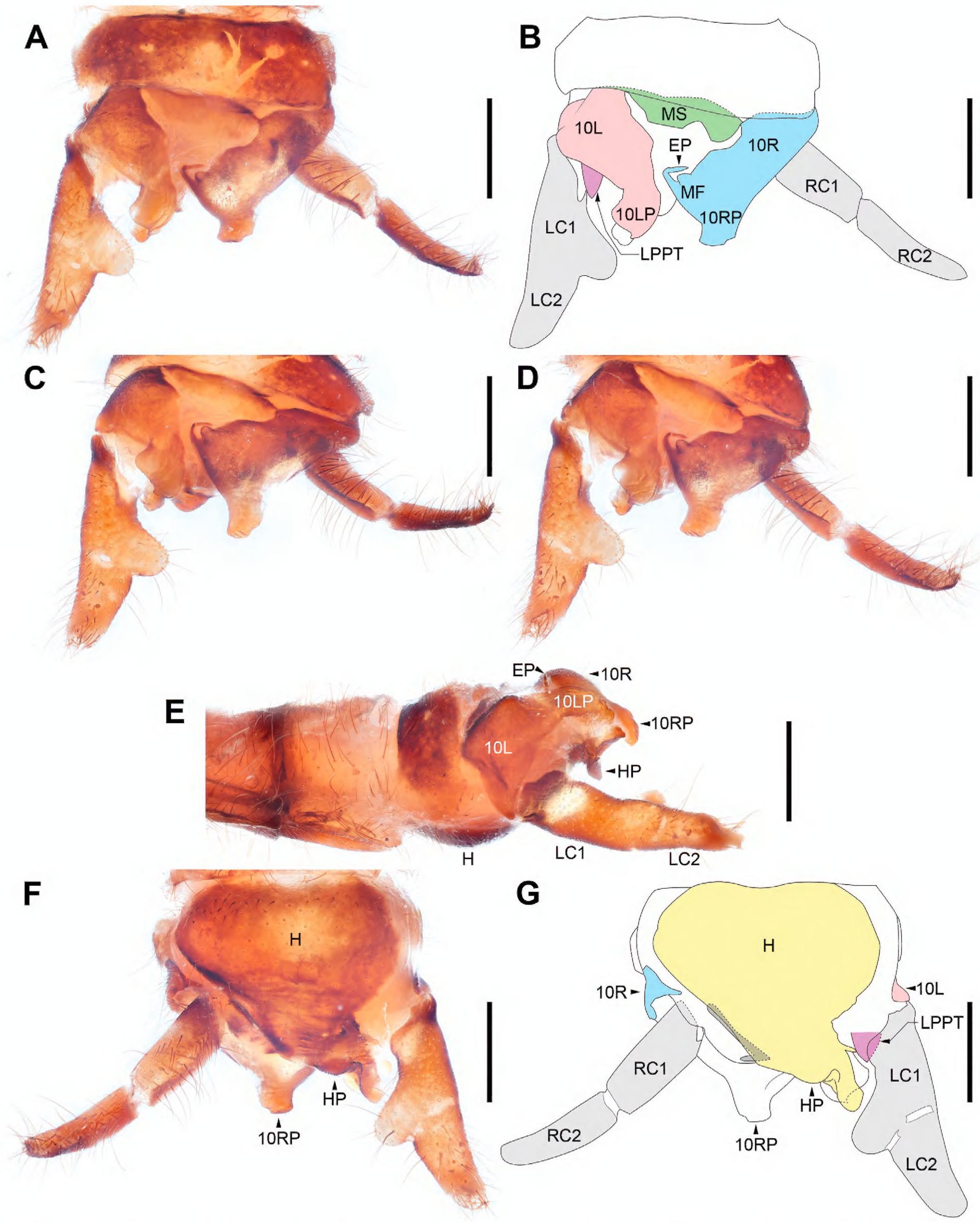

Figure 5. *Ptilocerembia qiului* sp. nov., male holotype. **A.** Terminalia, dorsal view; **B.** Drawing of terminalia, dorsal view; **C.** Terminalia, slightly dorsocaudal view; **D.** Terminalia, dorsolateral view; **E.** Terminalia, lateral view; **F.** Terminalia, ventral view; **G.** Drawing of terminalia, ventral view. Abbreviation: 10L/R – left/right hemitergite of abdominal segment 10; 10LP/RP – left/right hemitergal process; EP – epiproct; H – hypandrium (ninth sternite); HP – hypandrium process; LPPT – left paraproct; LC1/2 – first/second segment of left cercus; MF – medial flap; MS – medial sclerite; RC1/2 – first/second segment of right cercus. Scale bars: 0.5 mm.

strong bias toward A/T-ending codons; the most frequent codons encode serine (UCU, UCA) and threonine (ACC) (see Suppl. material 2: fig. S1A).

Analysis of selective pressure (Ka/Ks) for each PCG (vs. *P. lanyuhensis*) yielded values < 1.0 for all genes (see Suppl. material 2: fig. S1B), indicating overall purifying

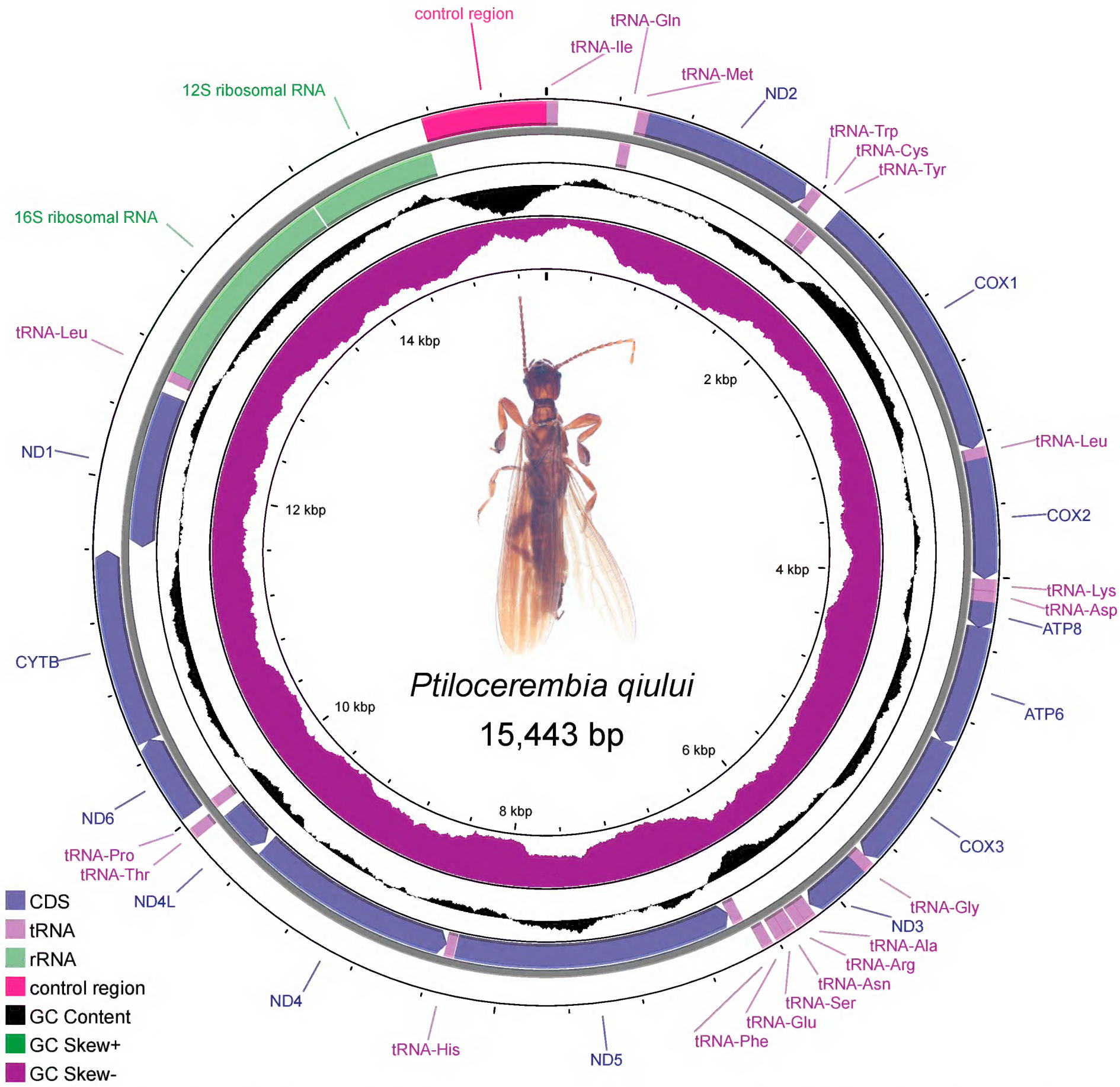

Figure 6. *Ptilocerembia qiului* sp. nov., mitochondrial map. Genes outside the map are transcribed in a clockwise direction, whereas those inside the map are transcribed counterclockwise. The second circle shows the GC content, and the third shows the GC skew. GC content and GC skew are plotted as the deviation from the average value of the entire sequence.

selection in the sequenced webspinners. COX1 shows the lowest Ka/Ks (highest conservation), while ATP8 shows a relatively higher rate (although still <1). The pattern that COX1 is the slowest-evolving mitochondrial gene and an ATP synthase gene is the fastest is consistent with other Embioptera (Chen et al. 2017).

Molecular delimitation and phylogeny

The COX1 barcode of *P. qiului* sp. nov. was compared to six available *Ptilocerembia* sequences from GenBank (except for *P. senathami*, for which COX1 is missing). Pairwise K2P distances between *P. qiului* sp. nov. and other congeners ranged from 0.1259 to 0.1759 (see Suppl. material 2: fig. S2), far exceeding the widely adopted intraspecific thresholds (~2%) in webspinners and other insects (Hebert et al. 2003; Chen 2022, 2023). The smallest distance among any congeners was 0.042 (between *P. catherinae* and *P. thaidina*). In phylogenetic trees (BI, NJ, and ML), *P. qiului* sp. nov. grouped with two unnamed *Ptilocerembia* specimens sequenced in Miller et al. (2012), rather than with any of the formally described species. The phylogenetic placement of the new species was supported by relatively strong topological values, with a posterior probability of 0.82 in the BI tree (Fig. 7), a bootstrap value of 66 in the NJ tree (see Suppl. material 2: fig. S3A), and a bootstrap value of 52 in the ML tree (see Suppl. material 2: fig. S3B). These results indicate that the sequenced individual of *P. qiului* sp. nov. forms a distinct clade, consistent with its morphological uniqueness. In summary, both morphological and COX1 data support the delimitation of *P. qiului* sp. nov. as a new species, divergent from its congeners.

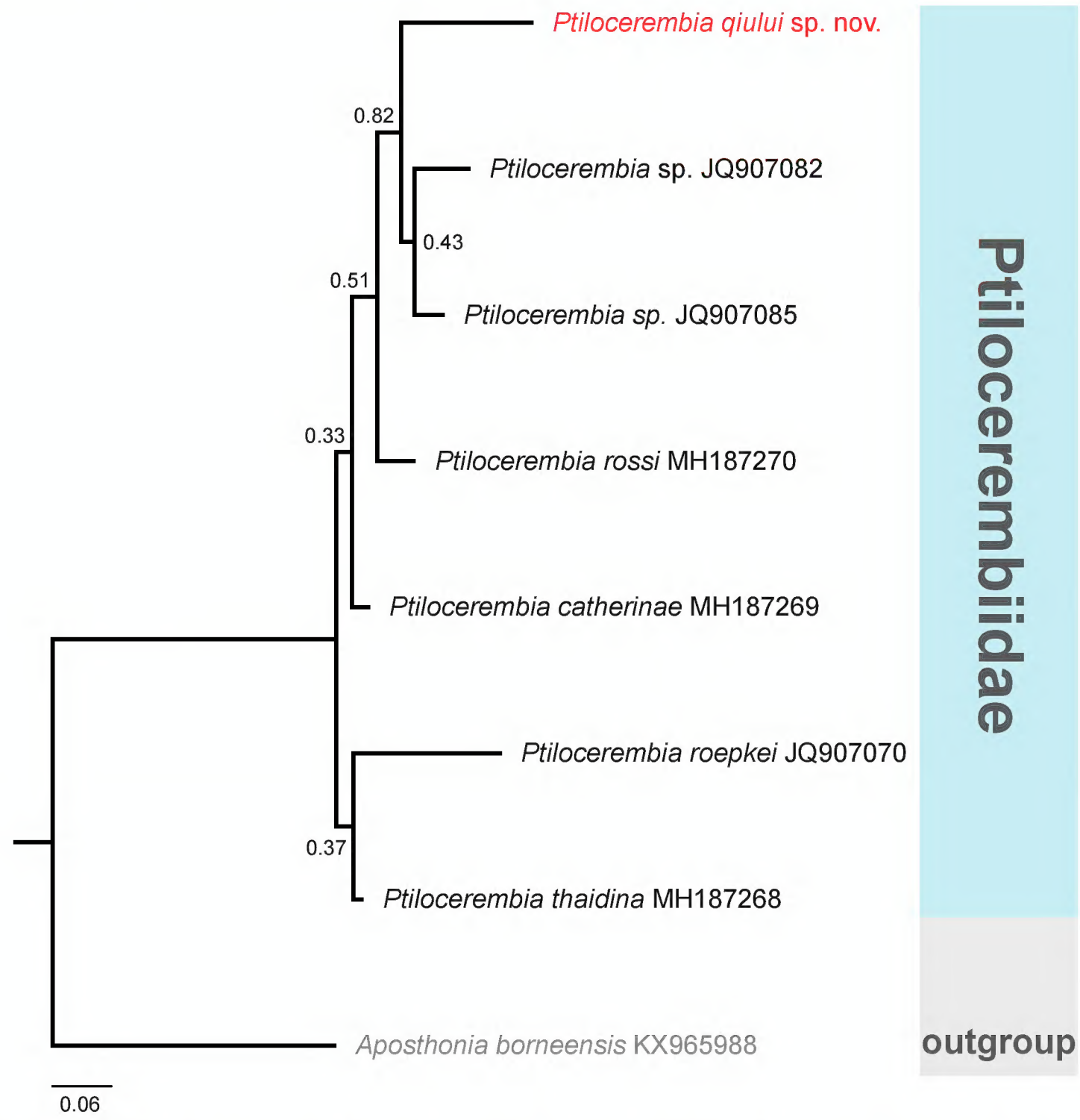

Figure 7. Bayesian inference tree of *Ptilocerembia* species based on COX1 sequences. Numbers at the nodes are posterior probabilities.

Discussion

This study reports the first record of the webspinner family Ptilocerembiidae from China, expanding the known range of this Southeast Asian lineage. *Ptilocerembia* was previously known from Indonesia through Thailand and Myanmar. The discovery of *P. qiului* sp. nov. in Yunnan Province (southwestern China) is consistent with the prediction of Ross (2007) that the montane regions of northern Myanmar, Laos, Vietnam, and southwestern China harbor undiscovered embiopteran taxa. Our finding extends the boundary of Ptilocerembiidae and suggests that related species may occur across the border regions in Indochina. Although this record is not the northernmost known occurrence of the genus (since Myanmar already hosted species of *Ptilocerembia*), it nonetheless highlights the broader biogeographic significance of Yunnan Province as a biodiversity hotspot. The presence of this lineage in Yunnan underscores the incompleteness of current knowledge of the embiopteran fauna in China.

Morphologically, *P. qiului* sp. nov. is clearly distinct from all described *Ptilocerembia* species, especially in the characters of its head and male genitalia. The combination of features (e.g., submentum shape, tergal processes, hypandrium form) distinguishes it from the four Thai species (Poolprasert and Edgerly 2014) and the Indonesian *P. roepkei*. In our analysis of molecular data, the COX1 barcode of *P. qiului* sp. nov. was highly divergent from those of all sampled congeners. The substantial interspecific distances (>0.12) far exceed usual DNA barcoding thresholds (Hebert et al. 2003) and indicate that the new specimens are not conspecific with any previously sequenced taxon. The congruence of morphological and genetic results provides strong evidence that the Chinese specimens represent a new species.

Notably, the genetic analysis revealed considerable interspecific genetic distances, suggesting that the specimens sequenced but not formally named in Miller et al. (2012) might also represent new species. The relatively small number of described species (currently six worldwide) combined with our findings implies that *Ptilocerembia* diversity is seriously underestimated. Many additional species likely remain to be discovered in Asia. Ross (1963) suspected a complex of many species across the region, and our results confirm that even putative colonies in well-surveyed areas can yield new taxa.

The complete mitogenome of *P. qiului* sp. nov. provides a first look at the mitogenomics of Ptilocerembiidae. It conforms to the typical insect pattern (13 PCGs, A+T-biased, ancestral gene order), but with some distinctive features. In particular, we found tandem repeats in a coding-region intergenic spacer (between trnI and trnQ)

that have not been reported in other webspinner mitogenomes. Tandem repeat regions are common in the control region of many insect mitogenomes, but their presence in this non-control region suggests lineage-specific evolution. The functional significance of these repeats is unclear. They could be neutral structural features or potentially involved in replication dynamics. In addition, two tRNA genes (trnV and trnS2) were not detected in our mitogenome assembly. Because missing tRNAs are sometimes the result of annotation or sequencing limitations rather than true gene loss (Morrison 2010), these absences should be interpreted cautiously until confirmed by additional sequencing data. Further comparative mitogenomic analyses of *Ptilocerembia* and related taxa will help clarify whether these features represent lineage-specific modifications or methodological artifacts. Our Ka/Ks analysis indicated that all protein genes are evolving under strong purifying selection (Ka/Ks < 1), with COX1 being the most conserved and ATP8 the least. The elevated Ka/Ks in ATP8 suggests a relaxed constraint on this gene, whereas COX1's strong constraint supports its use as a robust barcode marker.

Our study is based on male specimens from a single locality; no females are yet known for this species. More fieldwork is needed to collect females and additional populations of *P. qiului* sp. nov., which would allow for the study of potential intraspecific variation and female morphology. From a molecular perspective, our phylogenetic analysis used only COX1, which is useful for species delimitation but limited for deeper relationships. Future work should incorporate additional loci (nuclear markers or transcriptomes) and full mitogenomes of multiple species to build a more comprehensive phylogeny of Ptilocerembiidae and Embioptera. In particular, multi-gene phylogenomics could test the monophyly of Ptilocerembiidae and clarify its position relative to other families. Expanding genomic resources will also enable studies of population genetics and biogeography; for example, the tandem repeats found here could serve as genetic markers if conserved in populations.

In conclusion, we provide the first Chinese record of Ptilocerembiidae with the description of *P. qiului* sp. nov. Our integrative approach (morphology + mitogenomics) demonstrates the value of combining data types in embiid taxonomy. This discovery highlights the hidden diversity of webspinners and underscores that even well-studied regions can yield novel taxa. As taxonomic work progresses, it will be important to integrate classical morphology, DNA barcoding, and genomic data to achieve a robust classification of Embioptera and to document the evolutionary history of this insect order.

Acknowledgments

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Supplementary material 1

Supplementary tables

Authors: Zhi-Teng Chen, Yuan Xiong, Chao Jiang
Data type: xlsx
Explanation note: **table S1.** Comparison of diagnostic characters in *Ptilocerembia* species. **table S2.** Mitogenome organization of *Ptilocerembia qiului* sp. nov.
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Link: https://doi.org/10.3897/dez.72.170313.suppl1

Supplementary material 2

Supplementary figures

Authors: Zhi-Teng Chen, Yuan Xiong, Chao Jiang
Data type: pdf
Explanation note: **fig. S1.** *Ptilocerembia qiului* sp. nov., mitogenomic features. **A.** Relative synonymous codon usage (RSCU) of PCGs in the mitogenome; numbers on bars represent the ratio of each amino acid; **B.** Nonsynonymous/synonymous substitution (Ka/Ks) ratios of each PCG in three sequenced webspinner mitogenomes. **fig. S2.** Genetic distance among the DNA barcodes of *Ptilocerembia* species. **fig. S3.** Phylogenetic trees of *Ptilocerembia* species based on COX1 sequences. **A.** Neighborjoining tree; numbers at the nodes are bootstrap values; **B.** Maximum likelihood tree; numbers at the nodes are bootstrap values.
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